

## PERSPECTIVE OPEN



# Force of infection: a determinant of vaccine efficacy?

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Vaccine efficacy (VE) can vary in different settings. Of the many proposed setting-dependent determinants of VE, force of infection (FoI) stands out as one of the most direct, proximate, and actionable. As highlighted by the COVID-19 pandemic, modifying FoI through non-pharmaceutical interventions (NPIs) use can significantly contribute to controlling transmission and reducing disease incidence and severity absent highly effective pharmaceutical interventions, such as vaccines. Given that NPIs reduce the FoI, the question arises as to if and to what degree FoI, and by extension NPIs, can modify VE, and more practically, as vaccines become available for a pathogen, whether and which NPIs should continue to be used in conjunction with vaccines to optimize controlling transmission and reducing disease incidence and severity.

npj Vaccines (2021)6:51; https://doi.org/10.1038/s41541-021-00316-5

## INTRODUCTION

Lower apparent vaccine efficacy (VE) in low resource settings, when compared to VE observed in high resource settings, has been reported for several pathogens, most notably poliovirus, typhoid, and rotavirus<sup>1-5</sup>. Observed VE also varied when evaluating a malaria vaccine candidate in different parasite transmission settings<sup>6–8</sup>. Numerous economic, social, and biological factors have been proposed to explain these settingdependent variations in VE<sup>3,9–11</sup>. Many, if not most, of the proposed economic and social determinants of VE, such as, country income status, living conditions, access to healthcare, appear to act indirectly and non-specifically on VE; whereas many but not all biological factors, such as co-infections, malnutrition, and enteropathy, presumably act directly and proximally on VE. More practically, identification of direct and proximal determinants of setting-dependent VE that hold the promise of actionable intervention(s) seem a most urgent need in efforts to enhance and/or sustain VE.

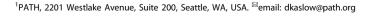
The COVID-19 pandemic has highlighted the contribution of non-pharmaceutical interventions (NPIs) in controlling transmission and reducing disease incidence and severity<sup>12</sup> particularly in the absence of highly effective pharmaceutical interventions, such as vaccines. NPIs also contribute to controlling other major human diseases, including use of condoms for HIV/AIDS<sup>13</sup>, bed nets for malaria<sup>14</sup>, and hand washing for diarrhea<sup>15</sup>. By reducing the number of (susceptible) individuals effectively contacted by each (infected) person, e.g., through physical barriers, distancing, and masking, NPIs reduce  $\lambda$ , the force of infection (FoI) (see Box 1, Glossary of Key Terms). As vaccines become available for a pathogen, the question arises as to if and which NPIs should continue to be used, if not prioritized<sup>16</sup>. This then begs the broader useinspired scientific question, as raised previously<sup>8</sup>: after optimizing the vaccine immunogen, formulation, dose level, and regimen, what remaining determinants of VE are amenable to intervention? More specifically, given the role of NPIs in reducing the Fol, if and to what degree is Fol, and by extension NPIs, a determinant of VE?

## Interrogating the potential relationship of FoI and settingdependent VE

A two-step approach was taken to interrogate the potential relationship between Fol and VE. The first explored three mathematical scenarios of VE as a function of various Fol settings. The second followed up on the decades-old observations of lower apparent efficacy of oral poliovirus<sup>1</sup> and oral typhoid vaccines<sup>5</sup> in low resource settings when compared to high resource settings. This empiric interrogation assessed the correlation between the incidence of disease in the placebo population (as a surrogate of Fol in the study population) and the observed VE in different geographical settings. Recent Phase 3 studies of malaria and rotavirus vaccine candidates across a number of settings, including low and high resource settings<sup>6,17</sup>, provided data for empirically assessing if and how Fol might be a determinant of VE.

Both the thought experiment of setting-dependent VE of a hypothetical vaccine and the retrospective analyses of rotavirus and malaria Phase 3 efficacy results make a multitude of assumptions that limit the robustness and soundness of any conclusions. For simplicity, factors previously shown or hypothesized to influence transmission, susceptibility, VE, and/or Fol, such as, country income status, age, underlying medical conditions, coinfections, access to healthcare, seasonality, NPI use, spreading events, and strain differences across different settings, and preexposure effect were excluded from consideration in both the hypothetical VE or observed VE analyses.

Given these significant limitations in the analyses, the primary goal of the present study was not to provide a definitive answer to the questions of if and to what degree Fol determines VE in different settings. Rather the goal of these analyses was to continue to raise the awareness of the potential impact of Fol on VE<sup>8,18</sup>, and to prompt prospective studies designed to assess if and how NPIs might reduce Fol and enhance VE when vaccines are introduced and scaled up. Ultimately well-designed studies that directly evaluate the potential relationship of Fol and setting-dependent VE will provide the evidence needed for well-informed policy recommendations on the continued use or not of NPIs during vaccine introduction and scale-up.









#### Box 1 Glossary of key terms

*Force of infection:* Rate at which susceptible individuals in a population acquire an infectious disease in that population, per unit time. It is also known as the incidence rate or hazard rate <sup>36</sup>.

$$\lambda_t = \frac{c_e l_t}{N_t} \tag{1}$$

(see equation 2.13, ref.  $^{36}$ ) where  $\lambda_t$  is the force of infection at time t,  $c_e$  is the number of individuals effectively contacted by each person per unit time,  $l_t$  is the number of infected in the population at time t, and  $N_t$  is the number in the population at time t.

Efficacy: The direct protection provided by vaccination against a defined clinical endpoint; it excludes any indirect (herd) effect<sup>36</sup>. Vaccine efficacy reflects the relative reduction between the vaccinated and control groups for one or more specific clinical endpoints. Calculations of the relative reduction typically use a hazard ratio, a risk ratio, or most simply, as shown below, an incidence ratio<sup>37</sup>;

$$VE = \frac{ARU - ARV}{ARU} \times 100 = 1 - \frac{\frac{I_V}{N_V}}{\frac{I_V}{N_U}} \times 100$$
 (2)

(see equations, ref.  $^{36}$ ) where VE is the vaccine efficacy, ARU is the attack rate in the unvaccinated population, ARV is the attack rate in the vaccinated population,  $I_V$  is the number of infected in the vaccinated population,  $N_V$  number in the vaccinated population,  $I_U$  is the number of infected in the unvaccinated population, and  $N_U$  is the number in the unvaccinated population.

*Herd immunity:* The proportion of a population immune to infection or disease<sup>2,36</sup>.

Herd immunity threshold: The proportion of the population required to be immune in the population for the infection incidence to reach steady state, i.e., the infection level is neither growing nor declining. To eliminate an infection in the population, the proportion of the population that is immune to infection must exceed this threshold value<sup>36</sup>.

*Indirect (Herd) effect:* The reduction in the rate of infection or disease in the unimmunized portion of a population as a result of immunizing a proportion of the population<sup>2</sup>.

# Three scenarios of the potential mathematical consequences of Fol on setting-dependent VE

The potential effects of FoI on the level of VE were explored in three mathematical scenarios: (1)  $VE_{constant}$ , where VE is independent of FoI; (2)  $VE_{linear}$ , where VE decreases linearly as a function of increasing FoI; and, (3)  $VE_{natural\ log}$ , where VE decreases logarithmically as a function of increasing FoI. As noted above, multiple simplifying assumptions were made when considering the mathematical consequences of FoI on VE, including homogeneity in the population with respect to a number of factors, such as, pathogen transmission, host susceptibility to infection and disease (be it genetic or acquired), FoI over time in a specific setting, and protective immunity as a result of vaccination across settings.

With these simplifying assumptions in mind, equations that define the three mathematical scenarios (see Box 2, VE as a function of Fol) are shown graphically in Fig. 1, using the example of a hypothetical vaccine that has a maximum VE of 83% studied under conditions of Fol that vary across two orders of magnitude, from 0.03 to 3.50 infections/person-year. While other more complex mathematical relationships between VE and Fol merit consideration, these three simple equations seemed a reasonable starting point from which to interrogate observed data from Phase 3 VE studies conducted in multiple epidemiological settings.

## Empiric evidence of Fol on observed setting-dependent VE

Results from recent placebo-controlled Phase 3 studies of vaccine candidates for two diverse pathogens, *Plasmodium falciparum* and rotavirus, provided a database to determine which, if any, of the three mathematical scenarios best explained any setting-dependent differences in VE. The selection of malaria and diarrhea

#### Box 2 Vaccine efficacy as a function of force of infection

The following equations define mathematical relationships between vaccine efficacy (VE) and force of infection (Fol) shown in Fig. 1, when the relationship of VE is: (1) independent of Fol (VE $_{constant}$ ); (2) linear to Fol (VE $_{linear}$ ); or (3) logarithmic to Fol (VE $_{natural loo}$ ):

$$VE_{constant}: VE_{S} = -0 * \textbf{Fol}_{S} + VE_{max}$$
 (3)

$$VE_{linear}: VE_S = - \left( \frac{\textit{Fol}_S - Fol_{min}}{Fol_{max} - Fol_{min}} \right) \times \left( VE_{max} - VE_{min} \right) + VE_{max} \tag{4}$$

$$VE_{natural\,log}: VE_S = - \left( \frac{In\, \textit{Fol}_S - In\, Fol_{min}}{In\, Fol_{max} - In\, Fol_{min}} \right) \times \left( VE_{max} - VE_{min} \right) + VE_{max} \tag{5}$$

Where  $VE_S$  is the VE in setting S,  $VE_{max}$  is the highest observed VE, and  $VE_{min}$  is the lowest observed VE.

And where  $Fol_5$  is the Fol in setting S,  $Fol_{min}$  is the lowest observed Fol, and  $Fol_{max}$  is the highest observed Fol.

as clinical endpoints provided an opportunity to analyze Fol and VE for both vector-transmitted and fecal-oral-transmitted pathogens, as well as parenterally and orally administered vaccine candidates, respectively. In addition to the assumptions mentioned above, several additional assumptions noted below facilitated the analyses of these multi-setting VE studies of two pathogens.

First and foremost, the analyses of both pathogens assumed that the intent-to-treat (ITT) incidence of the most sensitive definition of the mildest disease endpoint in the youngest age cohort in the placebo arm best served as an internal Phase 3 study surrogate of  $\lambda$ , the Fol. The validity of this assumption relies upon several other assumptions, including the absence of any significant herd effect (see Box 1, Glossary of Key Terms) on the control from the vaccinated arm of the Phase 3 study. The rationale for making this herd effect assumption, typically also assumed for the control group used in estimating VE in the context of Phase 3 efficacy studies, relies upon: (1) the relatively small proportion of the total population in the study setting enrolled in the vaccinated group in the Phase 3 study; and, (2) the timing of incident disease in the control group relative to eliciting herd immunity and reaching the herd immunity threshold (see Box 1, Glossary of Key Terms) in the study population.

A third key assumption relied upon a comparison of trendlines from the three mathematical scenarios described above to the closest fit trendline of observed VE (VE<sub>observed</sub>) as a function of observed FoI (Fol<sub>observed</sub>, incidence in the placebo group) in each epidemiologic setting to determine if and how VE varied as a function of FoI. In this regard, because the Phase 3 VE results for both pathogens were known a priori to vary by epidemiologic setting, the posterior probability was low of selecting the VE<sub>constant</sub> mathematical scenario to categorize VE<sub>observed</sub> as a function of Fol<sub>observed</sub>. As noted below for each specific analysis, the observed trendline may not necessarily reflect a statistically significant association between VE<sub>observed</sub> and Fol<sub>observed</sub>, as assessed by a regression analysis.

## Malaria parasite VE and Fol

A single pivotal Phase 3 VE study (NCT00866619) enrolled 15,459 participants in two age categories (young children aged 5–17 months and infants aged 6–12 weeks at the time of enrollment) across 11 clinical research sites in seven African countries (one site in Burkina Faso, Gabon, Malawi, and Mozambique; two sites in Ghana and Tanzania; and three sites in Kenya). The trial assessed, as a primary aim, VE of a three-dose regimen of RTS,S/ASO1<sub>E</sub> against clinical malaria

Fol<sub>min</sub>: 0.03

Folmay: 3.50

Fol 0.03

0.06

0.10

0.30

0.66

1.00

2.33

3.50

Fol<sub>min</sub>: 0.03

Folmax: 3.46

0.03

0.08

0.20

0.21

0.71

2.02

2.06

3.04

3.46

Folo

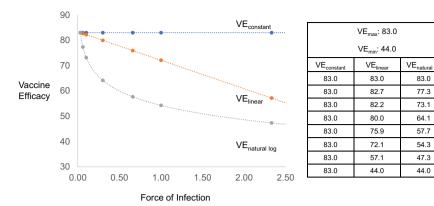


Fig. 1 Vaccine Efficacy (VE) as a function of force of Infection (FoI) for hypothetical vaccine. Equations that define three mathematical scenarios (see Box 2, Vaccine efficacy as a function of force of infection) are shown graphically, using as an example a hypothetical vaccine with a maximum vaccine efficacy (VE<sub>max</sub>) of 83.0% and minimum VE (VE<sub>min</sub>) of 44.0% studied under conditions of force of infection (FoI) that vary across two orders of magnitude, from a minimum FoI (FoI<sub>min</sub>) 0.03 to a maximum FoI (FoI<sub>max</sub>) of 3.50 infections/ person-year.

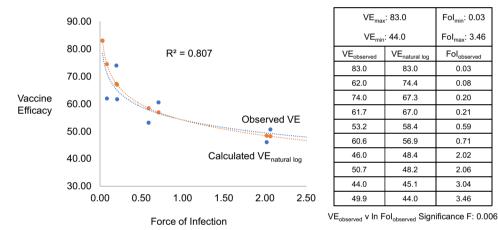


Fig. 2 Vaccine Efficacy (VE) as a function of Force of Infection (FoI) for malaria vaccine. Best fit trendline analysis of observed vaccine efficacy (VE<sub>observed</sub>) as a function of observed force of infection (Fol<sub>observed</sub>) is shown as a logarithmic relationship (blue dotted line) with a R<sup>2</sup> of 0.807. A regression analysis of VE<sub>observed</sub> as a function of In Fol<sub>observed</sub> shown in the embedded table has a Significance F of 0.006. Using the VE<sub>natural log</sub> equation (see Box 2, Vaccine efficacy as a function of force of infection), the observed VE<sub>max</sub>, VE<sub>min</sub>, Fol<sub>max</sub>, Folmin, and Folobserved were used to calculate the VEnatural log in the embedded table and the calculated VEnatural log shown graphically (orange dotted line).

over 12 months follow-up<sup>7</sup>. In the per-protocol population of the 5-17 months age category, VE<sub>observed</sub> was 51.3% (95% CI: 47.5–54.9; p-value < .0001) with a VE<sub>observed</sub> range from 83.0% (95% CI: 37.2-95.4; p-value 0.0079) in a low parasite transmission site (Kilifi, Kenya) to 44.0% (95% CI: 36.8-50.3; p-value <.0001) in a high parasite transmission site (Nanoro, Burkina Faso) (see Annex 6 Table 23, ref. 19). As noted above, the intent-to-treat (ITT) incidence of the more sensitive secondary definition of clinical malaria in the control group of infants aged 6-12 weeks at the time of enrollment (see Annex 7 Table 177, ref. <sup>20</sup>.) served as the internal Phase 3 study Fol<sub>observed</sub>, the surrogate of  $\lambda$  in the analyses.

The best fit trendline analysis of VE<sub>observed</sub> as a function of Fol<sub>observed</sub> revealed a logarithmic relationship (Fig. 2, Observed VE) with an  $R^2$  of 0.807. Regression analysis of VE<sub>observed</sub> as a function of In Fol<sub>observed</sub> revealed a Significance F of 0.006. Using the  $VE_{natural\ log}$  equation (Box 2), the observed  $VE_{max}$ , VE<sub>min</sub>, Fol<sub>max</sub>, Fol<sub>min</sub>, and the Fol<sub>observed</sub> from each site generated a logarithmic relationship between the calculated

site-specific VE and Folobserved (Fig. 2, Calculated VE). These analyses suggest that malaria parasite Fol functions as a determinant of RTS,S/AS01<sub>E</sub> VE.

#### Rotavirus VE and Fol

Multiple Phase 3 studies of two rotavirus vaccines, RV1 (Rotarix") and RV5 (RotaTeq"), evaluated VE in diverse epidemiologic settings<sup>17</sup>. In comparison to the analyses conducted for malaria VE, the analyses of rotavirus VE<sub>observed</sub> as a function of rotavirus Folobserved was complicated by the evaluation of two different vaccine candidates, with two different regimens, in several different clinical protocols. Some of the Phase 3 studies conducted in low resource settings did not collect data on the incidence of rotavirus gastroenteritis (RVGE) of any severity. The analyses excluded these studies due to the absence of an intent-to-treat incidence of any severity RVGE in the placebo group to serve as a surrogate of  $\lambda$ . The analyses also excluded data from countries in which the placebo group



Table 1. Rotavirus vaccine Phase 3 study settings by country, World Bank country income classification, and surrogate observed force of infection. Country (RV#) NTC References Economy FOI<sub>observed</sub> 39 **Finland** Н 16.3 RV5 Not available 24,40 Brazil UM 16 1 RV1 NCT00140673 26.41 Malawi 14.4 RV1 NCT00241644 24.40 Mexico UM RV1 NCT00140673 13.8 South Africa UM 122 RV1 NCT00241644 27 EU/USA Н 11.2 RV5 NCT00092443 23,42 China UM 106 RV1 NCT01171963 22.43 France Н 10.0 RV1 NCT00140686 25.44 Japan Н 10.0 RV1 NCT00480324 22.43 Finland Н 8.8 RV1 NCT00140686 28 Japan Н 7.1 RV5 NCT00718237 Ghana LM 7.1 RV5 NCT00362648 24.40 UM Venezuela 6.0 RV1 NCT00140673 31 China UM RV5 NCT02062385 5.4 22,43 Czech Republic RV1 Н 4.1 NCT00140686 29 Kenya LM 3.7 RV5 NCT00362648 32 Bangladesh I M RV5 NCT00362648 n/a 32 Vietnam RV5 NCT00362648 LM n/a <sup>a</sup> See ref. <sup>21</sup>

had no or just a single case of RVGE of any severity. From those studies that collected sufficient incidence of any severity RVGE in the placebo group, an Analysis of Variance failed to detect a statistically significant difference (*p*-value = 0.749) when categorizing Folobserved by 2020 World Bank country income classifications (i.e., upper- v upper middle- v lower middle/lower-income country)<sup>21</sup> (Table 1).

For RV1, results from 10 countries in five independent Phase 3 studies<sup>17,22–26</sup> (see Table 1) met the above Fol<sub>observed</sub> criteria for interrogation. The best fit trendline analysis of  $VE_{observed}$  as a function of Folobserved revealed a linear relationship (Fig. 3a upper line, Observed VE) with an  $R^2$  of 0.3892 and regression analysis with a Significance F of 0.158. The VE<sub>observed</sub> of 94.9% in one setting (Mexico) with Folobserved of 13.79 appeared to be a significant outlier. Reanalysis absent the data from Mexico revealed a linear relationship (Fig. 3a middle line, Observed VE), with an R<sup>2</sup> of 0.6264 and regression analysis Significance F of 0.0449. Using the VE<sub>linear</sub> equation (Box 2), the observed VE<sub>max</sub>, VE<sub>min</sub>, Fol<sub>max</sub>, Fol<sub>min</sub>, and the Fol<sub>observed</sub> from each of the 10 countries generated a linear relationship between the calculated site-specific VE and Folobserved (Fig. 3a lower line, Calculated VE). These analyses suggest that rotavirus Fol may function as a determinant of RV1 VE.

For RV5, results from five settings in three independent Phase 3 studies  $^{17,27-31}$  (see Table 1) met the above Fol<sub>observed</sub> criteria for interrogation. The best fit trendline analysis of VE<sub>observed</sub> as a function of Fol<sub>observed</sub> revealed an independent relationship (data not shown but provided for review) with an  $R^2$  of -0.215 and regression analysis Significance F of 0.9838. Interrogating results from 7 settings in five independent Phase 3 studies  $^{17,27-32}$  (see Table 1) by using the incidence of SRVGE in the placebo group as the Fol<sub>observed</sub> and surrogate of  $\lambda$  in the analyses, the best fit trendline analysis of VE<sub>observed</sub> as a function of Fol<sub>observed</sub> revealed a linear relationship (Fig. 3b, Observed VE) with an  $R^2$  of 0.6692 and regression analysis Significance F of 0.081. Using the VE<sub>linear</sub> equation (Box 2), the observed VE<sub>max</sub>, VE<sub>min</sub>, Fol<sub>max</sub>, Fol<sub>min</sub>, and the Fol<sub>observed</sub> from

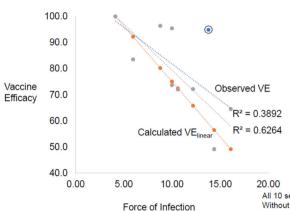
each of the 7 settings in the reanalysis generated a linear relationship between the calculated site-specific VE and Fol<sub>observed</sub> (Fig. 3b lower line, Calculated VE). These analyses suggest that rotavirus Fol may function as a determinant of RV5 VE, when the incidence of SRVGE, rather than RVGE of any severity, in the placebo group serves as the Fol<sub>observed</sub> in the analyses.

## CONCLUSION

That a relationship between Fol and VE appears logarithmic for a parenterally administered malaria vaccine candidate and linear for two orally administered rotavirus vaccine candidates may reflect different routes of infection, routes of vaccine administration, fold differences between the Fol<sub>max</sub> and Fol<sub>min</sub> (i.e., more than a hundred-fold for malaria and less than tenfold for rotavirus) or other differences between the pathogens, host responses, or vaccines. If a causal relationship rather than an indirect (e.g., pre-exposure effect<sup>33</sup>), misleading<sup>34</sup>, or chance association between Fol and VE exists, then of the many proposed determinants of setting-dependent VE, Fol provides one of the most direct, mechanistically proximate potential determinants. Furthermore, for many but not all pathogens, modifying the Fol provides one of the most actionable interventions to enhance or sustain VE. While improving indirect or distal VE determinants, such as poverty, gut pathology, co-infections, malnutrition, and the microbiome<sup>35</sup> could significantly enhance efforts to control and eliminate simultaneously many pathogens, implementing interventions that effectively mitigate these VE determinants is complex and not immediately achievable. In contrast, modifying the Fol through the concomitant use of affordable, accessible, available, acceptable, and sustainable NPIs provides a proximate and actionable approach to optimizing VE. Considering and then prospectively verifying the speculation that introduction or continued optimal use of NPIs in an effort to reduce the Fol and thereby enhance or sustain VE,



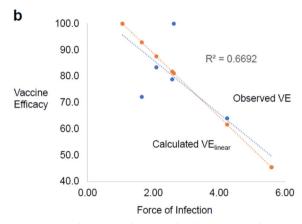
## VE SVRGE v Any RVGE Fol (RV1)



VE <sub>max</sub> : 100		Fol <sub>min</sub> : 4.11
VE <sub>min</sub> : 49.2		Fol <sub>max</sub> : 16.11
VE <sub>observed</sub>	VE <sub>linear</sub>	Fol
100	100	4.11
83.6	92.2	5.96
96.4	80.2	8.79
73.7	75.1	10.00
95.4	75.1	10.00
72.0	72.5	10.62
72.2	65.8	12.19
94.9	59.0	13.79
49.2	56.5	14.38
64.5	49.2	16.11

All 10 settings: VE<sub>observed</sub> v FoI<sub>observed</sub> Significance F: 0.158 Without Mexico: VE<sub>observed</sub> v FoI<sub>observed</sub> Significance F: 0.0449

## VE SVRGE v SRVGE Fol (RV5)



VE <sub>max</sub> : 100		Fol <sub>min</sub> : 1.06
VE <sub>min</sub> : 45.4		Fol <sub>max</sub> : 5.60
VE <sub>observed</sub>	VE <sub>linear</sub>	Fol
100	100	1.06
72.2	92.9	1.65
83.4	87.6	2.09
78.8	81.8	2.58
100	81.2	2.62
64.0	61.6	4.25
45.4	45.4	5.60

VE<sub>observed</sub> v Fol<sub>observed</sub> Significance F: 0.081

**Fig. 3 Vaccine Efficacy (VE) as a function of Force of Infection (Fol) for rotavirus vaccines. a** RV1: Best fit trendline analysis of observed vaccine efficacy (VE<sub>observed</sub>) as a function of observed force of infection (Fol<sub>observed</sub>) is shown as a linear relationship for all 10 countries (blue dotted line) and for 9 countries (exclusion of the outlier, encircled blue dot; gray dotted line) with a  $R^2$  of 0.3892 and 0.6264, respectively. Regression analyses of VE<sub>observed</sub> as a function of Fol<sub>observed</sub> in the embedded table have Significance Fs of 0.158 and 0.0449. Using the VE<sub>linear</sub> equation (see Box 2, Vaccine efficacy as a function of force of infection), the observed VE<sub>max</sub>, VE<sub>min</sub>, Fol<sub>max</sub>, FOl<sub>min</sub> and Fol<sub>observed</sub> were used to calculate the VE<sub>linear</sub> in the embedded table and the calculated VE<sub>linear</sub> shown graphically (orange dotted line). **b** RV5: Best fit trendline analysis of observed vaccine efficacy (VE<sub>observed</sub>) as a function of observed force of infection (Fol<sub>observed</sub>) is shown as a linear relationship (blue dotted line) with a  $R^2$  of 0.6692. A regression analysis of VE<sub>observed</sub> as a function of Fol<sub>observed</sub> in the embedded table has a Significance F of 0.081. Using the VE<sub>linear</sub> equation (see Box 2, Vaccine efficacy as a function of force of infection), the observed VE<sub>max</sub>, VE<sub>min</sub>, Fol<sub>max</sub>, Fol<sub>min</sub> and Fol<sub>observed</sub> were used to calculate the VE<sub>linear</sub> in the embedded table and the calculated VE<sub>linear</sub> shown graphically (orange dotted line).

respectively, upon vaccine rollout seems prudent and, in the context of a pandemic, quite urgent.

# Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

## **DATA AVAILABILITY**

All data used in the analyses can be publicly accessed. The sources and web links for all the data have been cited in the references.

## **CODE AVAILABILITY**

All analyses conducted using Microsoft Excel for Microsoft 365 version 2101.

Received: 21 January 2021; Accepted: 12 March 2021;

Published online: 12 April 2021

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#### **ACKNOWLEDGEMENTS**

The author thanks Dr. Marc Lipsitch for critical review and suggestions. This work was supported by the Bill & Melinda Gates Foundation, Seattle, WA [OPP1180199]. The funder had no role in the preparation of the manuscript or decision to publish.

### **AUTHOR CONTRIBUTIONS**

D.C.K. conceived, wrote, reviewed, approved and is accountable for this paper.

## **COMPETING INTERESTS**

D.C.K., an employee of PATH (a not-for-profit organization), has no financial interest in any for-profit organization, and declares no competing interests.

## **ADDITIONAL INFORMATION**

**Supplementary information** The online version contains supplementary material available at https://doi.org/10.1038/s41541-021-00316-5.

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